

<!--StartFragment-->RESULT 10

AFP31814

ID AFP31814 standard; cDNA; 301 BP.

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AC AFP31814;

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DT 18-OCT-2007 (first entry)

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DE Glycine max cDNA SEQ ID NO:122992.

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KW ss; gene; plant; cold tolerance; heat tolerance; drought resistance;

KW herbicide resistance; pathogen resistance; pesticide resistance;

KW disease-resistance; crop improvement; insect resistance;

KW nitrogen fixation; plant growth regulation; plant disease;

KW stress tolerance; seed oil; transgenic.

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OS Glycine max.

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PN US2004031072-A1.

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PD 12-FEB-2004.

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PF 28-APR-2003; 2003US-00424599.

XX

PR 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX

PA (LROS/) LA ROSA T J.

PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (CAOY/) CAO Y.

XX

PI La Rosa TJ, Zhou Y, Kovalic DK, Cao Y;

XX

DR WPI; 2004-168999/16.

XX

PT New recombinant DNA construct, useful in producing plants with desired
PT properties, e.g. increased cold, heat or drought tolerance or tolerance
PT to herbicides, extreme osmotic conditions or pathogens and improved plant
PT growth and development.

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PS Claim 1; SEQ ID NO 122992; 15pp; English.

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CC The invention relates to a recombinant DNA construct, polynucleotides or
CC polypeptides which are useful in improving plant cold, heat or drought
CC tolerance or tolerance to herbicides, extreme osmotic conditions,
CC pathogens or pests, in improving yield by modification of photosynthesis
CC or of carbohydrate, nitrogen or phosphorus use and/or uptake, in
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, in providing increased resistance to plant disease and improved
CC plant growth and development under at least one stress condition, in
CC producing galactomannan, plant growth regulators and lignin, in
CC increasing the rate of homologous recombination in plants, in modifying
CC seed oil yield and/or content and seed protein yield and/or content and
CC in encoding a plant transcription factor. The present sequence represents
CC a Glycine max cDNA of the invention. Note: This sequence is not shown in
CC the specification but was obtained in electronic format directly from
CC USPTO at seqdata.uspto.gov/sequence.html.

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SQ Sequence 301 BP; 111 A; 41 C; 70 G; 79 T; 0 U; 0 Other;

Query Match 100.0%; Score 12; DB 15; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCAGCGGAGTC 12
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Db 149 GCCAGCGGAGTC 160

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